

## SEQUENCE LISTING

<110> CABEZON SILIVA, Teresa Elisa Virginia  
ELLIS, Jonathan H.  
GERARD, Catherine Marie Ghislaine  
HAMBLIN, Paul A.  
PALMANTIER, Remi, M.  
VINALS Y DE BASSOLS, Carlota

<120> Immunogenic Compositions

<130> B45311

<140> To Be Assigned

<150> PCT/EP03/06096

<151> 2003-06-06

<150> GB 0213365.0

<151> 2002-06-11

<150> GB 0300914.9

<151> 2003-01-15

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<211> 429

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<213> Streptococcus pneumoniae

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<211> 336

<212> DNA

<213> Streptococcus pneumoniae

<400> 16

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<211> 1674

<212> DNA

<213> Homo sapiens

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<210> 18

<211> 1947

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and human P501S.

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<211> 1662

<212> DNA

<213> Artificial Sequence

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<223> Codon optimised human P501S

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<223> Codon optimised human P501S

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ccactacgac	gagggagtgc	gtatgggctc	cctgggcctc	ttcttgcaagt	gcgccatcag	1020
tctggttttc	tctctggtca	tggacaggct	ggtgcagcgc	ttcggaacct	gggcgggtgta	1080
cctggcgagc	gtggccgctt	tccccgtggc	tgcgggcgcc	acctgcctct	ctcactcggg	1140
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ccccctcct	gcgctgtgcg	gggccagcgc	ctgcgacgtg	agcgtgcgcg	tgggtggggg	1440
cgagcccacc	gaggcccgcg	tgggtccggg	cagaggcatt	tgtctggacc	tggccatcct	1500
cgactccgcc	ttctctctca	gccaggtggc	cccgtccctc	ttcatgggct	ctatcgtcca	1560
gctgtctcag	agcgtcaccg	cttacatggt	gtccgctgct	ggactgggct	tgggtggctat	1620
ttatttcgcc	accaggtgg	tgttcgacaa	gagcgacctg	gccaaatact	ccgcctgact	1680
cgaggcag						1688

<210> 22

<211> 1688

<212> DNA

<213> Artificial Sequence

<220>

<223> Codon optimised human P501S

<400> 22

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ggcccagttg	ctgctgggtga	acctgctgac	tttcggactg	gaggtgtgcc	tggctgcccg	120
gatcacgtac	gtgccccccc	tgctgctgga	ggtgggcgtg	gaggagaagt	tcatgacaat	180
ggtgctgggc	atcgcccccg	tcctgggcct	cgtgtgtgtg	cccctcctcg	ggagtgcgtc	240
cgatcattgg	cggggccgct	acggccgccg	cagaccgttc	atctgggccc	tgagcctggg	300
catcctgctc	tctctcttcc	tgatcccccg	ggccggctgg	ctggccggcc	tgctgtgtcc	360
cgacccccgc	cctctggagc	tggccctcct	gatcctgggc	gtgggcctgc	tggacttctg	420
cggccaggtg	tgtttcactc	ccctggaggc	tctgctctcc	gacctcttcc	gcgaccccga	480
ccactgtagg	caggcttaca	gcgtgtacgc	cttcatgac	agtctggggg	gatgcctggg	540
ctatctgctg	cccgtatcgc	actgggacac	cagcgccttg	gccccctacc	tggggactca	600
ggaggagtgc	ctgttcggcc	tgctcacctt	gatcttctcg	acgtgcgtcg	ccgccaccct	660
gctggtggcc	gaggaggcgg	ccctggggcc	caccgagccc	gccgagggcc	tgagcgctcc	720
cagcctgagc	ccccattgct	gcccgtgcag	ggctaggctc	gccttcagga	atctgggcgc	780
tttgctgcc	cgctgcacgc	agctgtgctg	tgcgatgcct	cgcaccctgc	gccgcctggt	840
cgtcgctgag	ctctgttcc	ggatggccct	gatgacgttc	accctcttct	acaccgactt	900
cgtgggggag	ggcctgtacc	agggcgtgcc	cagggccgag	cccggcaccg	aggctaggcg	960
ccattacgac	gagggcgtca	ggatgggctc	tctgggcctc	ttcctgcagt	gcgccatcag	1020
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cgccgtgggtg	accgccagcg	ccgccctgac	cggcttcacc	ttcagtgcgc	tccagattct	1200
gccctacacc	ctggcgcttc	tgtaccatcg	cgagaagcag	gtgttctctg	ccaagtaccg	1260



```

cggggacaca gggggagctt cctctgagga cagcctgatg accagcttct tgccccggccc 1320
caagccgggg gcccctttcc ccaacggcca tgtcggggcg ggcggcagcg gcctgctccc 1380
tcccccccc gcccgtgtcg gcgctagtgc ctgcgacgtg agcgtgcggg tgggtggtggg 1440
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cgactccgcc ttctgtctct cccaggtggc gccagcctg ttcattgggca gtatcgtgca 1560
gctgagccag agcgtgaccg cctacatggt gagcgccgcc ggcctggggg tgggtggccat 1620
ctactttgcc acccaggtcg tgttcgacaa gagcgatctc gccaaagtata gcgcctgact 1680
cgaggcag                                     1688

```

<210> 23

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S

<400> 23

```

atggcgggcg cttacgtaca ttccgacggc tcttatccaa aagacaagtt tgagaaaatc 60
aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggaggaag 120
cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
aaaatcgctg ataagtggta ctatttcaac gaagaaggtg ccatgaagac aggctgggtc 240
aagtacaagg aacttggta ctacttagac gctaaagaag gcgccatgca atacatcaag 300
gctaactcta agttcattgg tatcactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
gaaaagttca tgtac                                     435

```

<210> 24

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 24

```

atggccggcg cctacgtgca tagcgacggg agctacccca aggacaagtt cgagaagatc 60
aacgggacat ggtactactt cgactcctcc ggctacatgc tcgccgaccg ctggcggaag 120
cacaccgacg gcaactggta ctggttcgat aactcgggag agatggccac cggctggaag 180
aagatcgcgg acaagtggta ctatttcaac gaggagggcg ccatgaagac cggctgggtg 240

aagtataagg acacctggta ctacctcgac gccaaaggagg gcgccatgca gtatatcaag 300
gccaacagca agttcatcgg catcacccgag ggagtgatgg tcagcaacgc ctttatccag 360
agcgccgacg gcaccggatg gtactacttg aagccggacg gcaccctcgc ggatcgggcc 420
gagaagttca tgtac                                     435

```

<210> 25

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 25

```
atggccgccc cctacgtgca cagcgacggg tcctacccaa aggacaagtt cgagaagatc 60
aacggcacgt ggtactatct cgacagcagc ggctacatgc tcgccgatcg ctggcgcaag 120
cacaccgacg ggaactggta ctggttcgac aactctggcg agatggctac ggggtggaag 180
aagatcgccc acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240
aagtacaagg acacctggta ctacctggac gctaaggagg gcgccatgca gtacatcaag 300
gccaaactcga agttcatcgg gatcacccag ggcgtgatgg tcagtaacgc ttatcatccag 360
agcgcgggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagacct 420
gagaaattca tgtac                                     435
```

<210> 26

<211> 464

<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid gene between St. pneum. C-LytA, P2 T helper  
epitope and a small portion of the 5' end of human  
P501S - codon-optimised

<400> 26

```
gacggctagc gccaccatgg ccgccgccta cgtgcatagc gacgggagct accccaagga 60
caagttcgag aagatcaacg ggacatggta ctacttcgac tcctccggct acatgctcgc 120
cgaccgctgg cggaagcaca ccgacggcaa ctggtactgg ttcgataact cgggagagat 180
ggccaccggc tgggaagaaga tcgcgggaaa gtggtactat ttcaacgagg agggcgccat 240
gaagaccggc tgggtgaagt ataaggacac ctggtactac ctgcacgcca aggagggcgc 300
catgcagtat atcaaggcca acagcaagtt catcggcatc accgagggag tgatggtcag 360
caacgccttt atccagagcg ccgacggcac cggatggtac tacttgaagc cggacggcac 420
cctcgcggat cggcccga ga agttcatgta ctgactcgag gcag                                     464
```

<210> 27

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Hybrid protein between St. pneum. C-LytA, P2 T  
helper epitope and amino acids 51-553 of human  
P501S

<400> 27

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Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
 1           5           10           15
Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
      20           25           30
Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
      35           40           45
Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
      50           55           60
Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
      65           70           75           80
Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
      85           90           95
```

Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val		
			100					105					110				
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr		
		115					120					125					
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met		
	130					135					140						
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro		
145					150					155						160	
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg		
			165						170					175			
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe		
			180						185					190			
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro		
		195					200					205					
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp		
	210					215					220						
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp		
225					230					235					240		
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala		
			245						250					255			
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile		
		260					265						270				
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu		
		275					280					285					
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala		
	290					295					300						
Thr	Leu	Leu	Val	Ala	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala			
305					310					315				320			
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg		
			325						330					335			
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His		
			340					345					350				
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala		
		355					360					365					
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr		
	370					375					380						
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro		
385					390					395				400			
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser		
			405						410					415			
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val		
			420					425					430				
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala		
		435					440					445					
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His		
	450					455					460						
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe		
465					470					475				480			
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg		
			485						490					495			
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala		
		500						505					510				
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro		
		515					520					525					
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu		
	530					535					540						

Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
545					550					555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
				565					570					575	
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
			580					585					590		
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
		595					600					605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
	610					615					620				
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625					630					635					640
Lys	Tyr	Ser	Ala	Gly	His	His	His	His	His	His					
				645					650						

<210> 28  
 <211> 1959  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA encoding the Hybrid protein between St. pneum.  
 C-LytA, P2 T helper epitope and amino acids 51-553  
 of human P501S

<400> 28

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cacacagacg	gcaactggta	ctggttcgac	aactcaggcg	aaatggctac	aggctggaag	180
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aagtacaagg	acacttggtg	ctacttagac	gctaaagaag	gcgccatgca	atacatcaag	300
gctaactcta	agttcattgg	tatcactgaa	ggcgtcatgg	tatcaaattgc	ctttatccag	360
tcagcggacg	gaacaggctg	gtactacctc	aaaccagacg	gaacactggc	agacaggcca	420
gaaaagtcca	tgtacatggg	gctgggcatt	ggccagtgct	tgggcctggg	ctgtgtcccc	480
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tgggcactgt	ccttgggcat	cctgctgagc	ctctttctca	tcccaagggc	cggctggcta	600
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gggctgctgg	acttctgtgg	ccagggtgtg	ttcactccac	tggaggccct	gctctctgac	720
ctcttcgggg	acccggacca	ctgtcgccag	gcctactctg	tctatgcctt	catgatcagt	780
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ttcctgcccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	1560
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gtacgtgtgg	tggtgggtga	gcccaccgag	gccaggggtg	ttccgggccg	gggcatctgc	1740
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```

atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
ctgggtctgg tcgccattta ctttgctaca caggtagtat ttgacaagag cgacttggcc 1920
aaatactcag cgggtggaca ccatcaccat caccattaa 1959

```

```

<210> 29
<211> 507
<212> PRT
<213> Artificial Sequence

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<220>
<223> Human P501S (amino acids 55-553) fused to 6
      histidine residues

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```

<400> 29
Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu
 1          5          10          15
Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg
 20          25          30
Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu
 35          40          45
Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg
 50          55          60
Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe
 65          70          75          80
Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu
 85          90          95
Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe
100          105          110
Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp
115          120          125
Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys
130          135          140
Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr
145          150          155          160
Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu
165          170          175
Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala
180          185          190
Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln
195          200          205
Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu
210          215          220
Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp
225          230          235          240
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
245          250          255
Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu
260          265          270
Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met
275          280          285
Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser
290          295          300
Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser
305          310          315          320
Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser
325          330          335

```

Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu
			340					345					350		
Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala	Ser
		355					360					365			
Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro	Gly
	370					375					380				
Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu
385					390					395					400
Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val
				405				410						415	
Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly	Arg
			420					425					430		
Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser
		435					440					445			
Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln
	450					455					460				
Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val	Ala
465					470					475					480
Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala	Lys
				485				490						495	
Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His					
			500					505							

<210> 30

<211> 1524

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 55-553)  
fused to 6 histidine residues

<400> 30

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agtgaccact	ggcgtggacg	ctatggccgc	cgccggccct	tcatctgggc	actgtccttg	120
ggcatcctgc	tgagcctctt	tctcatccca	agggccggct	ggctagcagg	gctgtctgtgc	180
ccgatccca	ggcccctgga	gctggcactg	ctcatcctgg	gcgtggggct	gctggacttc	240
tgtggccagg	tgtgcttcac	tccactggag	gccctgctct	ctgacctctt	ccgggacccg	300
gaccactgtc	gccaggccta	ctctgtctat	gccttcatga	tcagtcttgg	gggctgcctg	360
ggctacctcc	tgccctgcat	tgactgggac	accagtggcc	tggcccccta	cctgggcacc	420
caggaggagt	gcctctttgg	cctgtctacc	ctcatcttcc	tcacctgcgt	agcagccaca	480
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gccctgcttc	cccggctgca	ccagctgtgc	tgccgcatgc	cccgcaccct	gcgccggctc	660
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ttcgtgggcg	aggggctgta	ccagggcgtg	cccagagctg	agccggggcac	cgaggccccg	780
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tccctggtct	tctctcttgt	catggaccgg	ctggtgcagc	gattcggcac	tcgagcagtc	900
tatttgccca	gtgtggcagc	tttccctgtg	gctgccgggtg	ccacatgcct	gtcccacagt	960
gtggccgtgg	tgacagcttc	agccgccctc	accgggttca	ccttctcagc	cctgcagatc	1020
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cgaggggaca	ctggaggtgc	tagcagtgag	gacagcctga	tgaccagctt	cctgccaggc	1140
cctaagcctg	gagctccctt	ccctaattga	cacgtgggtg	ctggaggcag	tggcctgctc	1200
ccacctccac	ccgcgctctg	cggggcctct	gcctgtgatg	tctccgtacg	tgtggtggtg	1260

```

ggtgagccca ccgaggccag ggtgggtccg ggccggggca tctgcctgga cctcgccatc 1320
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cagctcagcc agtctgtcac tgcctatatg gtgtctgccc caggcctggg tctggtcgcc 1440
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ggacaccatc accatcacca ttaa                                     1524

```

<210> 31

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Human P501S (amino acids 1-34 fused to 55-553)  
fused to 6 histidine residues

<400> 31

```

Met Ala Ala Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg
 1          5          10          15
Lys Ala Gln Leu Leu Val Asn Leu Thr Phe Gly Leu Glu Val
      20          25          30
Cys Leu Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp
      35          40          45
Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly
      50          55          60
Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr
      65          70          75          80
Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala
      85          90          95
Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp
      100          105          110
Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala
      115          120          125
Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly
      130          135          140
Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp
      145          150          155          160
Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe
      165          170          175
Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val
      180          185          190
Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg
      195          200          205
Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu
      210          215          220
Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp
      225          230          235          240
Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu
      245          250          255
Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser

      260          265          270
Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr
      275          280          285
Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala
      290          295          300
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
      305          310          315          320

```

Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	
				325					330					335		
Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	
				340				345					350			
Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	
		355					360					365				
Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	
	370					375					380					
His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	
385					390					395					400	
Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	
				405					410					415		
Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	
			420					425					430			
Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	
		435					440					445				
Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	
	450					455					460					
Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	
465					470					475					480	
Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	
				485				490						495		
His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	
			500				505						510			
Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	
	515					520						525				
Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	
	530					535					540					
Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	
545					550					555					560	
Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	
				565				570						575		
Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	
		580						585					590			
Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	
		595					600					605				
Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	
	610					615					620					
Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	
625					630					635					640	
Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	
				645				650						655		
Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	
			660				665						670			
Ala	Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
		675					680					685				

<210> 32

<211> 2058

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 1-34 fused to 55-553) fused to 6 histidine residues



<400> 32

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tccgacggct cttatccaaa agacaagttt gagaaaatca atggcacttg gtactacttt 180
gacagttcag gctatatgct tgcagaccgc tggaggaagc acacagacgg caactggtac 240
tggttcgaca actcaggcga aatggctaca ggctggaaga aaatcgctga taagtggtag 300
tatttcaacg aagaagggtgc catgaagaca ggctgggtca agtacaagga cacttggtag 360
tacttagacg ctaaagaagg cgccatgcaa tacatcaagg ctaactctaa gttcattggt 420
atcactgaag gcgtcatggt atcaaagtc tttatccagt cagcggacgg aacaggctgg 480
tactacctca aaccagacgg aacactggca gacaggccag aaaagttcat gtacatggtg 540
ctgggcattg gtccagtgtc gggcctggtc tgtgtcccgc tcctaggctc agccagtgtg 600
cactggcgtg gacgctatgg ccgcccggcg cccttcatct gggcactgtc cttgggcctc 660
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ttgtcgcccc actgctgtcc atgccggggc cgcttggtt tccggaacct gggcgccctg 1140
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gctgagctgt gcagctggat ggcactcatg accttcacgc tgttttacac ggatttcgtg 1260
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gccagtgtgg cagctttccc tgtggctgcc ggtgccacat gcctgtccca cagtgtggcc 1500
gtggtgacag cttcagccgc cctcaccggg ttcaccttct cagccctgca gatcctgccc 1560
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gacactggag gtgctagcag tgaggacagc ctgatgacca gcttcctgcc aggccctaag 1680
cctggagctc cttccctaa tggacacgtg ggtgctggag gcagtggcct gctcccacct 1740
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cccaccgagg ccagggtggt tccggggccg ggcattctgc tggacctcgc catcctggat 1860
agtgccttcc tgctgtccca ggtggcccca tccctgttta tgggtccat tgtccagctc 1920
agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt cgccatttac 1980
tttgctacac aggtagtatt tgacaagagc gacttgcca aatactcagc ggggtggacac 2040
catcacatc accattaa 2058
```

<210> 33

<211> 671

<212> PRT

<213> Artificial Sequence

<220>

<223> St. pneum. C-LytA portion fused to P2 T helper  
epitope fused to Human P501S (amino acids 55-553)  
fused to 6 histidine residues downstream of yeast  
alphaprepro signal sequence

<400> 33

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Met Ala Ala Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala
 1             5             10             15
Ser Ser Ala Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro
             20             25             30
Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser
             35             40             45
Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn
             50             55             60
```

Trp	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	65	70	75	80
Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	85	90	95	
Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	100	105	110	
Gly	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	115	120	125	
Glu	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	130	135	140	
Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	145	150	155	
Lys	Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	165	170	175	
Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	180	185	190	
Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	195	200	205	
Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	210	215	220	
Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	225	230	235	
Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	245	250	255	
Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	260	265	270	
Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	275	280	285	
Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	290	295	300	
Gln	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	305	310	315	
Val	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	325	330	335	
Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	340	345	350	
Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	355	360	365	
Arg	Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	370	375	380	
Phe	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	385	390	395	
Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	405	410	415	
Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	420	425	430	
Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	435	440	445	
Ser	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	450	455	460	
Tyr	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	465	470	475	
Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	485	490	495	
Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	500	505	510	
Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr				



```

tggtgagga ggcagcgctg ggccccaccg agccagcaga agggctgtcg gccccctcct 1500
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```

<210> 35

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Human P501S (amino acids 55-553) fused to 6  
histidine residues downstream of yeast alphaprepro  
signal sequence

<400> 35

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Met Ser Phe Leu Asn Phe Thr Ala Val Leu Phe Ala Ala Ser Ser Ala
 1          5          10          15
Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
 20          25          30
Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
 35          40          45
Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
 50          55          60
Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
 65          70          75          80
Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val
 85          90          95
Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp
 100         105         110
Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu
 115         120         125
Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala
 130         135         140
Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile
 145         150         155         160
Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro
 165         170         175
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg
 180         185         190

Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu
 195         200         205

```



<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 55-553)  
fused to 6 histidine residues downstream of yeast  
alphaneprepro signal sequence

<400> 36

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tcagatttag aaggggattt cgatgttgct gttttgccat tttccaacag cacaataaac 180
gggttattgt ttataaatac tactattgcc agcattgctg cttaaagaaga aggggtatct 240
ctcgagaaaa gagaggctga agccatgggtg ctgggcattg gtccagtgtc gggcctggtc 300
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gccctggccc cctacctggg caccaggag gagtgcctct ttggcctgct caccctcatc 720
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gatgtctccg tacgtgtggt ggtgggtgag cccaccgagg ccagggtggt tccgggccgg 1560
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gccgcaggcc tgggtctggt cgccatttac tttgctacac aggtagtatt tgacaagagc 1740
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<210> 37

<211> 1955

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding codon-optimised Human P501S (amino  
acids 51-553) fused to St.pneum. C-LytA P2 helper  
epitope C-Lyta

<400> 37

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ccaccggctg gaagaagatc gcggacaagt ggtactatct caacgaggag ggcgccatga 240
agaccggctg ggtgaagtat aaggacacct ggtactacct cgacgccaa gagggcgcca 300
tgcatatat caaggccaac agcaagttca tcggcatcac cgaggagtg atggtcagca 360
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tcgtgtgtgt	gcccctcctc	gggagtgcgt	ccgatcattg	gcggggccgc	tacggccgcc	540
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gggcccggctg	gctggccggc	ctgctgtgtc	ccgacccccg	ccctctggag	ctggccctcc	660
tgatcctggg	cgtgggcctg	ctggacttct	gcggccaggt	gtgtttcact	cccctggagg	720
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cgcccagcct	gttcatgggc	agtatcgtgc	agctgagcca	gagcgtgacc	gcctacatgg	1860
tgagcgccgc	cggcctgggg	ttggtggcca	tctactttgc	caccaggtc	gtgttcgaca	1920
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<210> 38

<211> 2045

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding codon-optimised Human P501S (amino acids 1-553)  
fused to St.pneum. C-Lyta P2 helper epitope C-Lyta

<400> 38

gcggccgcgc	caccatggcc	gccgcctacg	tgcatagcga	cgggagctac	cccaaggaca	60
agttcgagaa	gatcaacggg	acatggtact	acttcgactc	ctccggctac	atgctcgccg	120
accgctggcg	gaagcacacc	gacggcaact	ggtactggtt	cgataactcg	ggagagatgg	180
ccaccggctg	gaagaagatc	gcggacaagt	ggtactatct	caacgaggag	ggcgccatga	240
agaccggctg	ggtgaagtat	aaggacacct	ggtactacct	cgacgccaa	gagggcgcca	300
tgacgtatat	caaggccaac	agcaagttca	tcggcatcac	cgagggagt	atggtcagca	360
acgcctttat	ccagagcgcc	gacggcaccg	gatggtacta	cttgaagccg	gacggcacc	420
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aggcccagtt	gctgctggtg	aacctgctga	ctttcgact	ggagggtgtg	ctggctgccg	540
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tctactttgc	caccaggtc	gtgttcgaca	agagcgatct	cgccaagtat	agcgcctgag	2040
gatcc						2045

<210> 39

<211> 2105

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-LytA fused to Human P501S (amino acids 51-553)  
fused to Human P501S (amino acids 1-50) -  
Codon-optimised

<400> 39

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ccaccggctg	gaagaagatc	gcggacaagt	ggtactatct	caacgaggag	ggcgccatga	240
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acgcctttat	ccagagcgcc	gacggcaccg	gatggtacta	cttgaagccg	gacggcacc	420
tcgcggatcg	gcccagaga	ttcatgtaca	tggtgtctgg	catcgcccc	gtcctggggc	480
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gatcc 2105

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<210> 40

<211> 2105

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding Human P501S (amino acids 1-50) fused  
to St.pneum. C-LytA P2 helper epitope C-Lyta fused  
to Human P501S (amino acids 51-553) -  
Codon-optimised

<400> 40

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cccagttgct gctggtgaac ctgctgactt tcggactgga ggtgtgcctg gctgccggga 120
tcacgtacgt gccccccctg ctgctggagg tgggcgtgga ggagatggcc gccgcctacg 180
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gatcc 2105

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<210> 41  
 <211> 652  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to  
 Human P501S

<400> 41  
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 Phe Glu Lys Ile Asn Gly Thr Trp Tyr Phe Asp Ser Ser Gly Tyr  
 20 25 30  
 Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp  
 35 40 45  
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp  
 50 55 60  
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val  
 65 70 75 80  
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met  
 85 90 95  
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val  
 100 105 110  
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr  
 115 120 125  
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met  
 130 135 140  
 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro  
 145 150 155 160  
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg  
 165 170 175  
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe  
 180 185 190  
 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro  
 195 200 205  
 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp  
 210 215 220  
 Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp  
 225 230 235 240  
 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala  
 245 250 255  
 Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile  
 260 265 270  
 Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu  
 275 280 285  
 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala  
 290 295 300  
 Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala  
 305 310 315 320  
 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg  
 325 330 335  
 Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His  
 340 345 350  
 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala  
 355 360 365

Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
370						375					380				
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390					395					400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405					410					415	
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
			420					425					430		
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
	435						440					445			
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
450						455					460				
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
465					470					475					480
Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
				485					490					495	
Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
			500					505					510		
Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
		515					520					525			
Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
	530					535					540				
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545					550					555					560
Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
				565					570					575	
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu
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Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
		595					600					605			
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
	610					615					620				
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala
625					630					635					640
Lys	Tyr	Ser	Ala	Gly	Gly	His	His	His	His	His	His				
				645					650						

<210> 42

<211> 1959

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-LytA fused to Human P501S (plus his tag)

<400> 42

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cacacagacg	gcaactggta	ctggttcgac	aactcaggcg	aaatggctac	aggctggaag	180
aaaatcgctg	ataagtggta	ctatttcaac	gaagaagggtg	ccatgaagac	aggctgggtc	240
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gaaaagttca	tgtacatggt	gctgggcatt	ggtccagtgc	tgggcctggt	ctgtgtcccc	480

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ttcctgcccc aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc 1560
agcttctctg caggccctaa gcctggagct cccttcctta atggacacgt ggggtgctgga 1620
ggcagtgggc tgctcccacc tccaccgcgc ctctgcgggg cctctgcctg tgatgtctcc 1680
gtacgtgtgg tgggtgggtga gccaccgag gccaggggtg ttccgggccc gggcatctgc 1740
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atgggctcca ttgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
ctgggtctgg tcgccattta ctttgctaca caggtagtat ttgacaagag cgacttggcc 1920
aaatactcag cgggtggaca ccatcaccat caccattaa 1959

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<210> 43  
 <211> 553  
 <212> PRT  
 <213> Homo sapiens

<400> 43

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Gln	Leu	Leu	Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu
			20					25					30		
Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val
		35					40					45			
Glu	Glu	Lys	Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly
	50					55					60				
Leu	Val	Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly
65					70				75					80	
Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile
			85					90					95		
Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu
			100					105					110		
Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly
		115					120					125			
Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu
	130					135					140				
Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala
145					150				155					160	
Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr
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Leu	Leu	Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu



<400> 44

Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	Asp	Lys
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Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
			20					25					30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
		35					40					45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50					55					60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
65					70				75					80	
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
				85					90					95	
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
			100					105					110		
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
		115					120					125			
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
	130					135					140				
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
145					150					155					160
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
				165					170					175	
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
			180					185					190		
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
		195					200					205			
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210					215				220					
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
225					230				235					240	
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
				245					250					255	
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
			260					265					270		
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
		275					280					285			
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
	290					295					300				
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
305					310					315					320
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
				325					330					335	
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340					345					350		
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
		355					360					365			
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
	370					375					380				
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
385					390				395						400
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405					410					415	
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val



		115						120						125				
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met			
	130					135					140							
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro			
145				150						155					160			
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg			
				165					170					175				
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe			
			180					185					190					
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro			
		195					200					205						
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp			
	210					215					220							
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp			
225					230					235					240			
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala			
				245					250					255				
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile			
		260					265						270					
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu			
		275					280					285						
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala			
	290						295						300					
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala			
305					310					315					320			
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg			
				325					330					335				
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His			
			340					345					350					
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala			
		355					360					365						
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr			
	370					375					380							
Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro			
385					390					395					400			
Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser			
				405					410					415				
Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val			
			420					425					430					
Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala			
		435					440					445						
Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His			
	450					455					460							
Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe					



				565					570					575			
Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu		
			580					585					590				
Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser		
		595					600					605					
Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val		
	610					615					620						
Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp	Leu	Ala		
625					630					635					640		
Lys	Tyr	Ser	Ala														

<210> 46  
 <211> 694  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> St.pneum. C-LyTA P2 helper epitope C-Lyta fused to  
 Human P501S (amino acids 1-553)- codon optimised

<400> 46																	
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			20					25					30				
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp		
		35					40					45					
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp		
	50					55					60						
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val		
65					70				75						80		
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met		
			85						90					95			
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val		
			100					105					110				
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr		
		115					120					125					
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Met	Val	Gln		
	130					135					140						
Arg	Leu	Trp	Val	Ser	Arg	Leu	Leu	Arg	His	Arg	Lys	Ala	Gln	Leu	Leu		
145					150					155					160		
Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu	Ala	Ala	Gly		
				165					170					175			
Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val	Glu	Glu	Lys		
			180						185				190				
Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys		
	195						200					205					
Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly		
	210					215					220						
Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser		
225					230					235					240		
Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro		
			245						250					255			
Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu		
			260					265					270				

Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu		
		275					280					285					
Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val		
	290					295					300						
Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro		
305					310					315					320		
Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln		
				325					330					335			
Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val		
			340					345					350				
Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu		
		355					360					365					
Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro		
	370					375					380						
Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg		
385					390					395					400		
Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe		
				405					410					415			
Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe		
			420					425					430				
Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala		
		435					440					445					
Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met		
	450					455					460						
Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser		
465					470					475					480		
Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr		
				485					490					495			
Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu		
			500					505					510				
Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe		
		515					520					525					
Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr		
	530					535					540						
His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly		
545					550					555					560		
Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro		
				565					570					575			
Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser		
			580					585					590				
Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp		
		595					600					605					
Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val		
	610					615					620						
Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe		
625					630					635					640		
Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln		
				645					650					655			
Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly		
			660					665					670				
Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp		
		675					680					685					
Leu	Ala	Lys	Tyr	Ser	Ala												
	690																

<211> 694

<212> PRT

<213> Artificial Sequence

<220>

<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused to  
Human P501S (amino acids 51-553) fused to Human  
P501S (amino acids 1-50) - codon-optimised

<400> 47

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Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	Gly	Tyr
			20					25					30		
Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	Tyr	Trp
		35					40					45			
Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	Ala	Asp
	50					55					60				
Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	Trp	Val
65					70					75				80	
Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	Ala	Met
			85						90					95	
Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
			100					105					110		
Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
		115					120					125			
Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
	130					135					140				
Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
145				150						155					160
Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
			165					170						175	
Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
		180						185					190		
Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
		195					200					205			
Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210					215					220				
Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
225					230					235					240
Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
			245						250					255	
Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
		260						265					270		
Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
		275					280					285			
Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
	290					295					300				
Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
305					310					315					320
Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
			325						330					335	
Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340					345					350		
Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
		355					360					365			
Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr



Gln	Leu	Leu	Leu	Val	Asn	Leu	Leu	Thr	Phe	Gly	Leu	Glu	Val	Cys	Leu	
			20					25					30			
Ala	Ala	Gly	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val	
		35					40					45				
Glu	Glu	Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro	Lys	
	50					55					60					
Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser	Ser	
65					70					75					80	
Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp	
				85					90					95		
Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile	
			100					105					110			
Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr	Gly	
		115					120					125				
Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu	Gly	
	130					135					140					
Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	
145					150					155					160	
Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	
				165					170					175		
Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	
			180					185					190			
Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	
		195					200					205				
Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	
	210					215					220					
Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	
225					230					235					240	
Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	
				245					250					255		
Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	
			260					265					270			
Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	
		275					280					285				
Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	
	290					295					300					
Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	
305					310					315					320	
Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	
				325					330					335		
Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	
			340					345					350			
Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu		
		355					360				365					
Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	
	370					375					380					
Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	
385					390					395					400	
Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	
				405					410					415		
Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	
			420					425					430			
Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	
		435					440					445				
Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	
	450					455					460					
Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	

465					470					475					480
Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr
				485					490					495	
Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu
			500					505					510		
Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe
		515					520					525			
Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr
		530				535					540				
His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly
545				550					555					560	
Gly	Ala	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro
			565					570					575		
Lys	Pro	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser
			580				585					590			
Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp
		595				600					605				
Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val
610				615					620						
Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe
625				630					635						640
Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln
			645				650					655			
Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly
		660				665					670				
Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val	Phe	Asp	Lys	Ser	Asp
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Leu	Ala	Lys	Tyr	Ser	Ala										
690															

<210> 49  
 <211> 1971  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> DNA encoding Human MUC-1 fused to St.pneum. C-LytA  
 P2 helper epitope C-LytA

<400> 49

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cagagaagtt	cagtgccag	ctctactgag	aagaatgctg	tgagtatgac	cagcagcgta	180
ctctccagcc	acagcccgg	ttcaggctcc	tccaccactc	aggacagga	tgctactctg	240
gccccggcca	cggaaccagc	ttcagggtta	gctgccacct	ggggacagga	tgctacctcg	300
gtcccagtc	ccaggccagc	cctgggctcc	accaccccgc	cagcccacga	tgctacctca	360
gccccggaca	acaagccagc	cccgggctcc	accgcccccc	cagcccacgg	tgctacctcg	420
gccccggaca	ccaggccgcc	cccgggctcc	accgcccccc	cagcccacgg	tgctacctcg	480
gccccggaca	ccaggccgcc	cccgggctcc	accgcccccc	cagcccacgg	tgctacctcg	540
gccccggaca	ccaggccgcc	cccgggctcc	accgcccccc	cagcccacgg	tgctacctcg	600
gccccggaca	acaggccgcc	cttggcgtcc	accgcccccc	cagcccacgg	tgctacctcg	660
gcctcagggt	ctgcatcagg	ctcagcttct	actctgggtg	acaacggcac	ctctgccagg	720
gctaccacaa	ccccagccag	caagagcact	ccattctcaa	ttcccagcca	ccactctgat	780
actcctacca	cccttgccag	ccatagcacc	aagactgatg	ccagtagcac	tcaccatagc	840
acggtacctc	ctctcacctc	ctccaatcac	agcattcttc	cccagttgtc	tactgggggc	900

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tctttctttt tcctgtcttt tcacatttca aacctccagt ttaattcctc tctggaagat 960
cccagcaccg actactacca agagctgcag agagacattt ctgaaatggt tttgcagatt 1020
tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 1080
gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
gtgagtgatg tgccatttcc tttctctgcc cagctctggg ctggggtgcc aggctggggc 1260
atcgcgctgc tgggtgctggt ctgtgttctg gttgcgctgg ccattgtcta tctcattgcc 1320
ttggctgtct gtcagtgcgc ccgaaagaac tacgggcagc tggacatctt tccagcccgc 1380
gatacctacc atcctatgag cgagtacccc acctaccaca cccatgggcg ctatgtgccc 1440
cctagcagta ccgatcgtag cccctatgag aagggttctg caggtaatgg tggcagcagc 1500
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gtacattccg acggctctta tccaaaagac aagtttgaga aaatcaatgg cacttgggtac 1620
tactttgaca gttcaggcta tatgcttgca gaccgctgga ggaagcacac agacggcaac 1680
tggtactggt tcgacaactc aggcgaaatg gctacaggct ggaagaaaat cgctgataag 1740
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tggtactact tagacgctaa agaaggcgcc atgcaatata tcaaggctaa ctctaagtgc 1860
attggtatca ctgaaggcgt catggtatca aatgccttta tccagtcagc ggacggaaca 1920
ggctggtact acctcaaacc agacggaaca ctggcagaca ggccagaatg a 1971

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<210> 50

<211> 656

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MUC-1 fused to St.pneum. C-LytA P2 helper  
epitope C-Lyta

<400> 50

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115          120          125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130          135          140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145          150          155          160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
 165          170          175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
 180          185          190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
 195          200          205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
 210          215          220

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Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr	Ser	Ala	Arg
225					230					235					240
Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	Ile	Pro	Ser
				245					250					255	
His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser	Thr	Lys	Thr
			260					265					270		
Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu	Thr	Ser	Ser
	275						280					285			
Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser	Phe	Phe	Phe
	290					295					300				
Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser	Leu	Glu	Asp
305					310					315					320
Pro	Ser	Thr	Asp	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile	Ser	Glu	Met	
			325					330					335		
Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu	Ser	Asn	Ile
			340					345					350		
Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu	Ala	Phe	Arg
		355					360					365			
Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe	Asn	Gln	Tyr
	370					375					380				
Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser	Asp	Val	Ser
385					390					395					400
Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly	Ala	Gly	Val
				405					410					415	
Pro	Gly	Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val	Leu	Val	Ala
			420					425					430		
Leu	Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln	Cys	Arg	Arg
		435					440					445			
Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp	Thr	Tyr	His
	450					455					460				
Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg	Tyr	Val	Pro
465					470					475					480
Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser	Ala	Gly	Asn
				485					490					495	
Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	Ala	Ala	Thr	Ser
			500					505					510		
Ala	Asn	Leu	Met	Ala	Ala	Ala	Tyr	Val	His	Ser	Asp	Gly	Ser	Tyr	Pro
		515					520					525			
Lys	Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr	Phe	Asp	Ser
	530					535					540				
Ser	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn
545					550					555					560
Trp	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys
				565					570					575	
Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala	Met	Lys	Thr
			580					585					590		
Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp	Ala	Lys	Glu
		595					600					605			
Gly	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr
	610					615					620				
Glu	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr
625					630					635					640
Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu
				645					650					655	



<211> 2037  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> DNA encoding St.pneum. C-LytA P2 helper epitope  
C-Lyta fused to Human MUC-1

<400> 51  
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aaaatcaatg gcacttggtg ctactttgac agttcaggct atatgcttgc agaccgctgg 180  
aggaagcaca cagacggcaa ctggtactgg ttcgacaact caggcgaaat ggctacaggc 240  
tggaagaaaa tcgctgataa gtggtactat ttcaacgaag aaggtgccat gaagacaggc 300  
tggtcaagt acaaggacac ttggtactac ttagacgcta aagaaggcgc catgcaatac 360  
atcaaggcta actctaagtt cattggtatc actgaaggcg tcatggtatc aaatgccttt 420  
atccagtcag cggacggaac aggctggtac tacctcaaac cagacggaac actggcagac 480  
aggccagaaa tgacaccggg caccagctct cctttcttcc tgctgctgct cctcacagtg 540  
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tcggctaccc agagaagttc agtgcccagc tctactgaga agaattgctgt gagtatgacc 660  
agcagcgtac tctccagcca cagccccggt tcaggctcct ccaccactca gggacaggat 720  
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gtcacctcgg ccccggaaca caggccgccc ttggcgctcca ccgccccctc agtcacaaat 1140  
gtcacctcgg cctcaggctc tgcacaggc tcagcttcta ctctggtgca caacggcacc 1200  
tctgccaggg ctaccacaac cccagccagc aagagcactc cattctcaat tcccagccac 1260  
cactctgata ctctaccac ccttgccagc catagacca agactgatgc cagtagcact 1320  
caccatagca cggtagctcc tctcacctcc tccaatcaca gcacttctcc ccagttgtct 1380  
actggggtct ctttcttttt cctgtctttt cacatttcaa acctccagtt taattcctct 1440  
ctggaagatc ccagcaccga ctactacaa gagctgcaga gagacatttc tgaaatgttt 1500  
ttgcagattt ataaacaagg ggtttttctg ggcctctcca atattaagtt caggccagga 1560  
tctgtggtgg tacaattgac tctggccttc cgagaaggta ccatcaatgt ccacgacgtg 1620  
gagacacagt tcaatcagta taaaacggaa gcagcctctc gatataacct gacgatctca 1680  
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ccagcccggg atacctacca tcctatgagc gagtaccca cctaccacac ccatgggcgc 1920  
tatgtgcccc ctagcagtag cgatcgtagc ccctatgaga aggtttctgc aggtaatggt 1980  
ggcagcagcc tctcttacac aaaccagca gtggcagcca cttctgcaa cttgtag 2037

<210> 52  
<211> 678  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> St.pneum. C-LytA P2 helper epitope C-Lyta fused  
to Human MUC-1

<400> 52  
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Val His Ser Gln Val Gln Met Ala Ala Tyr Val His Ser Asp Gly

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Ser	Tyr	Pro	Lys	Asp	Lys	Phe	Glu	Lys	Ile	Asn	Gly	Thr	Trp	Tyr	Tyr		
		35					40					45					
Phe	Asp	Ser	Ser	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr		
	50					55					60						
Asp	Gly	Asn	Trp	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly		
65					70					75					80		
Trp	Lys	Lys	Ile	Ala	Asp	Lys	Trp	Tyr	Tyr	Phe	Asn	Glu	Glu	Gly	Ala		
			85						90					95			
Met	Lys	Thr	Gly	Trp	Val	Lys	Tyr	Lys	Asp	Thr	Trp	Tyr	Tyr	Leu	Asp		
		100						105					110				
Ala	Lys	Glu	Gly	Ala	Met	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile		
		115					120					125					
Gly	Ile	Thr	Glu	Gly	Val	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala		
	130					135					140						
Asp	Gly	Thr	Gly	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp		
145					150					155					160		
Arg	Pro	Glu	Met	Thr	Pro	Gly	Thr	Gln	Ser	Pro	Phe	Phe	Leu	Leu	Leu		
			165					170						175			
Leu	Leu	Thr	Val	Leu	Thr	Val	Val	Thr	Gly	Ser	Gly	His	Ala	Ser	Ser		
			180					185					190				
Thr	Pro	Gly	Gly	Glu	Lys	Glu	Thr	Ser	Ala	Thr	Gln	Arg	Ser	Ser	Val		
		195					200					205					
Pro	Ser	Ser	Thr	Glu	Lys	Asn	Ala	Val	Ser	Met	Thr	Ser	Ser	Val	Leu		
	210					215					220						
Ser	Ser	His	Ser	Pro	Gly	Ser	Gly	Ser	Ser	Thr	Thr	Gln	Gly	Gln	Asp		
225					230					235					240		
Val	Thr	Leu	Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr		
				245					250					255			
Trp	Gly	Gln	Asp	Val	Thr	Ser	Val	Pro	Val	Thr	Arg	Pro	Ala	Leu	Gly		
			260					265					270				
Ser	Thr	Thr	Pro	Pro	Ala	His	Asp	Val	Thr	Ser	Ala	Pro	Asp	Asn	Lys		
		275					280					285					
Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala		
	290					295					300						
Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly		
305					310					315				320			
Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro		
			325					330						335			
Ala	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly		
			340					345					350				
Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn	Arg		
		355					360					365					
Pro	Ala	Leu	Ala	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala		
	370					375					380						
Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr		
385					390					395				400			
Ser	Ala	Arg	Ala	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser			
			405					410					415				
Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser		
			420					425					430				
Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu		
		435					440					445					
Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser		
	450					455					460						

[illegible]